

SEQUENCE LISTING

<110> van Rooijen, Gijs  
Keon, Richard Glenn  
Boothe, Joseph  
Shen, Yin

<120> Commercial Production of Chymosin in Plants

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<170> PatentIn Ver. 2.0

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<212> DNA

<213> Bovine

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<221> CDS

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Gln Tyr Phe Val Ala Val Thr His Ala Ala Glu Ile Thr Arg Ile Pro	
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ctc tac aaa ggt aag tct ctc cgt aag gcg ctg aag gaa cat gga ctt	144
Leu Tyr Lys Gly Lys Ser Leu Arg Lys Ala Leu Lys Glu His Gly Leu	
35 40 45	
cta gaa gac ttc ttg cag aaa caa cag tat ggc atc agc agc aag tac	192
Leu Glu Asp Phe Leu Gln Lys Gln Gln Tyr Gly Ile Ser Ser Lys Tyr	
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tcc ggc ttc ggt gaa gtt gct agc gtg cca ctt acc aac tac ctt gat	240
Ser Gly Phe Gly Glu Val Ala Ser Val Pro Leu Thr Asn Tyr Leu Asp	
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Ser Gln Tyr Phe Gly Lys Ile Tyr Leu Gly Thr Pro Pro Gln Glu Phe	
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acc gtt ctc ttt gat act ggt tcc tct gac ttc tgg gtt ccc tct atc	336
Thr Val Leu Phe Asp Thr Gly Ser Ser Asp Phe Trp Val Pro Ser Ile	
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tac tgc aag agc aat gcc tgc aag aac cac caa aga ttc gat ccg aga	384
Tyr Cys Lys Ser Asn Ala Cys Lys Asn His Gln Arg Phe Asp Pro Arg	
115 120 125	
aag tcg tcc acc ttc cag aac tta ggc aaa ccc ttg tct ata cac tac	432
Lys Ser Ser Thr Phe Gln Asn Leu Gly Lys Pro Leu Ser Ile His Tyr	
130 135 140	
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Ser	Asn	Ile	Val	Asp	Ile	Gln	Gln	Thr	Val	Gly	Leu	Ser	Thr	Gln	Glu	
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cca	ggt	gat	gtc	ttc	acc	tat	gca	gaa	ttc	gat	ggc	atc	ctt	ggt	atg	576
Pro	Gly	Asp	Val	Phe	Thr	Tyr	Ala	Glu	Phe	Asp	Gly	Ile	Leu	Gly	Met	
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Leu	Thr	Pro	Ser	Ala	Tyr	Thr	Ser	Gln	Asp	Gln	Gly	Phe	Cys	Thr	Ser	
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<213> Bovine

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Leu	Tyr	Lys	Gly	Lys	Ser	Leu	Arg	Lys	Ala	Leu	Lys	Glu	His	Gly	Leu	35	40	45	
Leu	Glu	Asp	Phe	Leu	Gln	Lys	Gln	Gln	Tyr	Gly	Ile	Ser	Ser	Lys	Tyr	50	55	60	
Ser	Gly	Phe	Gly	Glu	Val	Ala	Ser	Val	Pro	Leu	Thr	Asn	Tyr	Leu	Asp	65	70	75	80
Ser	Gln	Tyr	Phe	Gly	Lys	Ile	Tyr	Leu	Gly	Thr	Pro	Pro	Gln	Glu	Phe	85	90	95	
Thr	Val	Leu	Phe	Asp	Thr	Gly	Ser	Ser	Asp	Phe	Trp	Val	Pro	Ser	Ile	100	105	110	
Tyr	Cys	Lys	Ser	Asn	Ala	Cys	Lys	Asn	His	Gln	Arg	Phe	Asp	Pro	Arg	115	120	125	
Lys	Ser	Ser	Thr	Phe	Gln	Asn	Leu	Gly	Lys	Pro	Leu	Ser	Ile	His	Tyr	130	135	140	
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Ser	Asn	Ile	Val	Asp	Ile	Gln	Gln	Thr	Val	Gly	Leu	Ser	Thr	Gln	Glu	165	170	175	
Pro	Gly	Asp	Val	Phe	Thr	Tyr	Ala	Glu	Phe	Asp	Gly	Ile	Leu	Gly	Met	180	185	190	
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Asp	Arg	Asn	Gly	Gln	Glu	Ser	Met	Leu	Thr	Leu	Gly	Ala	Ile	Asp	Pro	225	230	235	240
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Ala	Cys	Glu	Gly	Gly	Cys	Gln	Ala	Ile	Leu	Asp	Thr	Gly	Thr	Ser	Lys	275	280	285	
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Ala	Thr	Gln	Asn	Gln	Tyr	Gly	Glu	Phe	Asp	Ile	Asp	Cys	Asp	Asn	Leu	305	310	315	320
Ser	Tyr	Met	Pro	Thr	Val	Val	Phe	Glu	Ile	Asn	Gly	Lys	Met	Tyr	Pro	325	330	335	
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Gly Phe Gln Ser Glu Asn His Ser Gln Lys Trp Ile Leu Gly Asp Val				
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385		390		

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 tatccctaca aatttattat ttgttaaaca ttttcaaacc gcataaaatt ttatgaagtc 240  
 ccgtctatct ttaatgtagt ctaacatttt catattgaaa tatataattt acttaatttt 300  
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 caatataaac aaattcttta ccttaagaag gatttcccat tttatatttt aaaaatatat 420  
 ttatcaaata tttttcaacc acgtaaactc cataataata agttgtttca aaagtaataa 480  
 aatttaactc cataattttt ttattcgact gatcttaaag caacaccagc tgacacaact 540  
 agccattttt ttctttgaat aaaaaaatcc aattatcatt gtattttttt tatacaatga 600  
 aaatttcacc aaacaatcat ttgtggtatt tctgaagcaa gtcattgtat gcaaaattct 660  
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ccatctcaac ccacacacaa acacattgcc tttttcttca tcatcaccac aaccacctgt															1320
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tacctataaa tacctctaat atcactcact tctttcatca tccatccatc cagagtacta															1500
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aac ttc ctt aag tct ttc cct ttc tac gct ttc ctt tgt ttc ggt caa															1604
Asn Phe Leu Lys 5 Ser Phe Pro Phe Tyr 10 Ala Phe Leu Cys 15 Gly Gln															
tac ttc gtt gct gtt act cac gct gct gag atc acc cgc att cct ctc															1652
Tyr Phe Val 20 Ala Val Thr His Ala 25 Ala Glu Ile Thr Arg 30 Ile Pro Leu															
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Tyr Lys 35 Gly Lys Ser Leu Arg 40 Lys Ala Leu Lys Glu His Gly Leu Leu															
gaa gac ttc ttg cag aaa caa cag tat ggc atc agc agc aag tac tcc															1748
Glu Asp Phe Leu Gln Lys 55 Gln Gln Tyr Gly Ile 60 Ser Ser Lys Tyr Ser 65															
ggc ttc ggt gaa gtt gct agc gtg cca ctt acc aac tac ctt gat agt															1796
Gly Phe Gly Glu Val 70 Ala Ser Val Pro Leu 75 Thr Asn Tyr Leu Asp 80 Ser															
caa tac ttt ggg aag atc tac ctc gga acc ccg cct caa gag ttc acc															1844
Gln Tyr Phe Gly Lys 85 Ile Tyr Leu Gly 90 Thr Pro Pro Gln Glu 95 Phe Thr															
gtt ctc ttt gat act ggt tcc tct gac ttc tgg gtt ccc tct atc tac															1892
Val Leu Phe 100 Asp Thr Gly Ser 105 Ser Asp Phe Trp Val 110 Pro Ser Ile Tyr															
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Cys Lys 115 Ser Asn Ala Cys Lys 120 Asn His Gln Arg Phe 125 Asp Pro Arg Lys															
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Gly Asp Val 180 Phe Thr Tyr Ala 185 Glu Phe Asp Gly Ile 190 Leu Gly Met Ala															
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Tyr Pro 195 Ser Leu Ala Ser 200 Glu Tyr Ser Ile Pro 205 Val Phe Asp Asn Met															
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Met Asn Arg His Leu 210 Val 215 Ala Gln Asp Leu 220 Ser Val Tyr Met Asp 225															

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Arg Asn Gly Gln Glu Ser Met Leu Thr Leu Gly Ala Ile Asp Pro Ser  
230 235 240

tac tac aca gga tct ctt cac tgg gtt cca gtc act gtg cag cag tac 2324  
Tyr Tyr Thr Gly Ser Leu His Trp Val Pro Val Thr Val Gln Gln Tyr  
245 250 255

tgg caa ttc act gtg gac agt gtc acc atc agc ggt gtg gtt gtt gca 2372  
Trp Gln Phe Thr Val Asp Ser Val Thr Ile Ser Gly Val Val Val Ala  
260 265 270

tgt gaa ggt gga tgt caa gct atc ttg gat acc ggt acg tcc aag ctg 2420  
Cys Glu Gly Gly Cys Gln Ala Ile Leu Asp Thr Gly Thr Ser Lys Leu  
275 280 285

gtc gga cct agc agc gac att ctc aac att cag caa gct att gga gcc 2468  
Val Gly Pro Ser Ser Asp Ile Leu Asn Ile Gln Gln Ala Ile Gly Ala  
290 295 300 305

aca cag aac cag tac ggt gag ttt gac ata gat tgc gac aac ctt agc 2516  
Thr Gln Asn Gln Tyr Gly Glu Phe Asp Ile Asp Cys Asp Asn Leu Ser  
310 315 320

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325 330 335

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340 345 350

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Phe Gln Ser Glu Asn His Ser Gln Lys Trp Ile Leu Gly Asp Val Phe  
355 360 365

att cgt gag tac tac agc gtc ttt gac agg gcc aac aac ctc gtt ggg 2708  
Ile Arg Glu Tyr Tyr Ser Val Phe Asp Arg Ala Asn Asn Leu Val Gly  
370 375 380 385

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Leu Ala Lys Ala Ile  
390

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cgtgacggct tatggaatgc ttcaaatagt acaaaaacaa atgtgtacta taagactttc 2996

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Leu Tyr Lys Gly Lys Ser Leu Arg Lys Ala Leu Lys Glu His Gly Leu  
35 40 45  
Leu Glu Asp Phe Leu Gln Lys Gln Gln Tyr Gly Ile Ser Ser Lys Tyr  
50 55 60  
Ser Gly Phe Gly Glu Val Ala Ser Val Pro Leu Thr Asn Tyr Leu Asp  
65 70 75 80  
Ser Gln Tyr Phe Gly Lys Ile Tyr Leu Gly Thr Pro Pro Gln Glu Phe  
85 90 95  
Thr Val Leu Phe Asp Thr Gly Ser Ser Asp Phe Trp Val Pro Ser Ile  
100 105 110  
Tyr Cys Lys Ser Asn Ala Cys Lys Asn His Gln Arg Phe Asp Pro Arg  
115 120 125  
Lys Ser Ser Thr Phe Gln Asn Leu Gly Lys Pro Leu Ser Ile His Tyr  
130 135 140  
Gly Thr Gly Ser Met Gln Gly Ile Leu Gly Tyr Asp Thr Val Thr Val  
145 150 155 160  
Ser Asn Ile Val Asp Ile Gln Gln Thr Val Gly Leu Ser Thr Gln Glu  
165 170 175  
Pro Gly Asp Val Phe Thr Tyr Ala Glu Phe Asp Gly Ile Leu Gly Met  
180 185 190  
Ala Tyr Pro Ser Leu Ala Ser Glu Tyr Ser Ile Pro Val Phe Asp Asn  
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